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Le Duc, Diana; Spataru, Ana; Ceanga, Mihai; Zagrean, Leon; Schöneberg, Torsten; Toescu, Emil C.; Zagrean, Ana-maria

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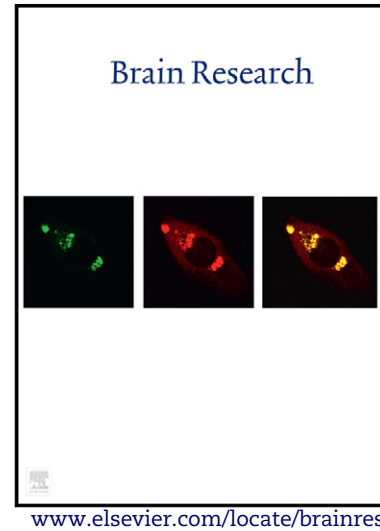
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**Developmental exposure to ethanol increases the neuronal
vulnerability to oxygen-glucose deprivation in cerebellar granule cell
cultures**

Diana Le Duc^{a,b,*1}, Ana Spataru^a, Mihai Ceanga^a, Leon Zagrean^a, Torsten

Schöneberg^b, Emil C. Toescu^c and Ana-Maria Zagrean^{a,*}

^aDivision of Physiology and Fundamental Neuroscience, Carol Davila University of
Medicine and Pharmacy, 050474 Bucharest, Romania

^bMolecular Biochemistry, Institute of Biochemistry, Medical Faculty, University of
Leipzig, Johannisallee 30, 04103 Leipzig, Germany

^cTranslational Neuroscience, School of Clinical and Experimental Medicine, College
of Medical and Dental Sciences, University of Birmingham, Birmingham B15 2TT,
United Kingdom

*Corresponding authors: Ana-Maria Zagrean, Division of Physiology and
Fundamental Neuroscience, Carol Davila University of Medicine and Pharmacy, 8
Eroii Sanitari Blvd., 050474 Bucharest, Romania. Tel/fax: 0040213120880. E-mail:
azagrean@umf.ro, azagrean@gmail.com

Diana Le Duc, Institute of Biochemistry, Medical Faculty, University of Leipzig,
Johannisallee 30, 04103 Leipzig, Germany; Tel: 004903419722175. E-mail:
diana_leduc@eva.mpg.de, diana.leduc@gmail.com

¹ Present Address: Molecular Biochemistry, Institute of Biochemistry, Medical Faculty, Leipzig
University, Johannisallee 30, 04103 Leipzig, Germany

22 Abstract

23 Prenatal alcohol exposure is associated with microencephaly, cognitive and
 24 behavioural deficits, and growth retardation. Some of the mechanisms of ethanol-
 25 induced injury, such as high level oxidative stress and overexpression of pro-
 26 apoptotic genes, can increase the sensitivity of fetal neurons towards
 27 hypoxic/ischemic stress associated with normal labour. Thus, alcohol-induced
 28 sequelae may be the cumulative result of direct ethanol toxicity and increased
 29 neuronal vulnerability towards metabolic stressors, including hypoxia. We examined
 30 the effects of ethanol exposure on the fetal cerebellar granular neurons' susceptibility
 31 to hypoxic/hypoglycemic damage. A chronic ethanol exposure covered the entire
 32 prenatal period and 5 days postpartum through breastfeeding, a time interval partially
 33 extending into the third-trimester equivalent in humans. After a binge-like alcohol
 34 exposure at postnatal day 5, glutamatergic cerebellar granule neurons were cultured
 35 and grown for 7 days *in vitro*, then exposed to a 3-hour oxygen-glucose deprivation to
 36 mimic a hypoxic/ischemic condition. Cellular viability was monitored by dynamic
 37 recording of propidium iodide fluorescence over 20 hours reoxygenation. We
 38 explored differentially expressed genes on microarray data from a mouse embryonic
 39 ethanol-exposure model and validated these by real-time PCR on the present model.
 40 In the ethanol-treated cerebellar granule neurons we find an increased expression of
 41 genes related to apoptosis (*Mapk8* and *Bax*), but also of genes previously described as
 42 neuroprotective (*Dhcr24* and *Bdnf*), which might suggest an actively maintained
 43 viability. Our data suggest that neurons exposed to ethanol during development are
 44 more vulnerable to *in vitro* hypoxia/hypoglycemia and have higher intrinsic death
 45 susceptibility than unexposed neurons.

46

47 **Highlights:**

48 - Fetal ethanol exposure increases neurons' vulnerability towards metabolic stressors

49 - Maternal alcoholism decreases offsprings' neuronal tolerance to hypoxia/ischemia

50 - Ethanol alters expression of genes associated with apoptosis and neuroprotection

51

52 **Keywords:** *prenatal ethanol exposure; oxygen-glucose deprivation; cerebellum;*

53 *neuronal vulnerability; differential gene expression.*

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55 **1 Introduction**

56 Prenatal alcohol exposure secondary to maternal ethanol consumption causes
 57 deleterious effects on fetal brain development (Falk, 2008). Even brief exposure to
 58 ethanol can result in growth retardation, craniofacial (Ismail et al., 2010) and systemic
 59 congenital abnormalities (Stratton, 1996). The damaging effects of ethanol on the
 60 developing nervous system have been thoroughly described since fetal alcohol
 61 syndrome was first investigated (Jones and Smith, 1975). The extent of neuronal
 62 impairment can lead accordingly to intellectual deficits, seizures, and even paraplegia
 63 (Streissguth and O'Malley, 2000). Fetal ethanol exposure determines an attenuation of
 64 hypoxic vasodilation that limits fetal oxygen delivery to the brain during hypoxic
 65 episodes (Mayock et al., 2007) and leads to altered glucose transport and metabolism
 66 (Fattoretti et al., 2003), promoting cellular damage during physiological peripartum
 67 hypoxia (Bakker and van Geijn, 2008). Moreover, chronic binge alcohol consumption
 68 has been shown to alter maternal uterine vascular function, leading to lowered blood
 69 supply to the placenta and consequently to the fetus (Subramanian et al., 2014).
 70 The cerebellum is highly sensitive to both, ethanol (Goodlett and Eilers, 1997) and
 71 hypoxia/ischemia (Cervos-Navarro et al., 1991; Goodlett and Eilers, 1997). Ethanol
 72 exposure during development causes an increased apoptotic cell death rate of both,
 73 cerebellar Purkinje and granule cells (Bhave and Hoffman, 1997), responsible for the
 74 severe motor impairments commonly associated with cerebellar dysfunction

Abbreviations

BAL, blood alcohol level; CGCs, cerebellar granule cells; C_T, cycle threshold; Ctr, control; EM+/-G, experimental medium with/without glucose; EtOH, ethanol; GO, gene ontology; OGD, oxygen-glucose deprivation; PI, propidium iodide; qPCR, quantitative polymerase chain reaction.

(Goodlett and Eilers, 1997). Neonatal cerebellum in rats shows a clear temporal window of vulnerability during the first 10 days after birth, a period corresponding to Purkinje cell dendritic outgrowth and synaptogenesis and to the third pregnancy trimester in humans (Dobbing and Sands, 1979; Goodlett et al., 1990). Within this period, cerebellar granule cells (CGCs) display a higher susceptibility to ethanol on postnatal days 4-6 (Goodlett et al., 1998), when proliferation of CGCs precursors towards postmitotic cells still occurs (Luo, 2012) and even short ethanol exposures can lead to significant loss of cerebellar neurons by intricate mechanisms such as inhibition of neurotrophic action, decrease in the pro-survival CREB binding protein expression (Guo et al., 2011), increased oxidative stress (Kotch et al., 1995), and activation of pro-apoptotic pathways (Light et al., 2002).

We investigated whether and how ethanol exposure influences the neuronal response to hypoxia/ischemia. Thus, CGCs cultures obtained from pups exposed to ethanol during fetal life and until postnatal day 5 were used in an *in vitro* oxygen-glucose deprivation (OGD) model. The model allows the evaluation of neurons' *in vitro* maturation after an *in vivo* ethanol exposure, which intercepts the maximum cerebellar vulnerability to ethanol, before the completion of neurite formation. Acute and delayed neuronal vulnerability secondary to OGD was assessed by a 20 hours-dynamic measurement of cellular death using propidium iodide (PI) fluorometry. Our data suggest that neurons exposed to ethanol during development are more vulnerable to *in vitro* hypoxia/hypoglycemia. To check whether our results are confirmed on a molecular level and to support a possible *in vivo* extrapolation of the results, we further analyzed gene expression profiles from publicly available microarray data in a mouse model of embryonic ethanol exposure. This revealed several biological pathways that showed differential regulation after ethanol exposure, including

embryonic organ and neuronal morphogenesis. Additionally, we validated genes by real-time PCR on the *in vitro* CGC model and identified some candidate genes which could be responsible for the low adaptive response to hypoxia/hypoglycemia of cerebellar granule cells derived from pups exposed to ethanol during the brain growth spurt period.

2 Results

2.1 Morphological assessment

Morphology and cell maturation of cultured CGCs were assessed in phase-contrast microscopy. There were no obvious morphological differences between cultures originating from ethanol-treated and non-treated animals (Fig. 1A). The morphological assessment at the end of the reoxygenation protocol revealed the nature and the extent of damage induced by OGD and/or ethanol pretreatment (Fig. 1B). Phase-contrast microscopy showed an increased level of cell injury in ethanol-exposed neurons, ranging from cytoplasmic swelling, loss of phase-bright contours, and intercellular connections in ethanol control group cultures, to loss of membrane integrity and the presence of multiple cell ghosts in the ethanol-treated cultures exposed to OGD (Fig. 1B). Cell death was confirmed on the same microscopic fields by PI fluorescence (Fig. 1B).

2.2 The response of ethanol-treated neurons to oxygen-glucose deprivation

We first assessed the effects of ethanol pre-exposure on the neuronal response to an OGD protocol. Neuronal viability at the end of a 3-h OGD exposure before the initiation of reoxygenation was measured by PI fluorescence. Figure 2A indicates that ethanol-treated neurons showed a significantly higher susceptibility to OGD exposure ($7.0 \pm 2.0\%$ cell death, $n = 5$) comparing to non-treated neurons exposed to OGD

124 (0.65 \pm 0.10% cell death, n = 4), p-value = 0.03. In the groups maintained in control
 125 normoxic/normoglycemic conditions, there was also a small but significant difference
 126 in survival between the non-treated control neurons and ethanol control neurons (0.26
 127 \pm 0.05% cell death, n = 4 and 0.62 \pm 0.09% cell death, n = 6, respectively, p-
 128 value = 0.01).

129 Reoxygenation at the end of the OGD period resulted in additional neuronal death,
 130 with an increased death in the non-treated population at 20 h of reoxygenation (Fig.
 131 2B). Figure 2B also shows that the increased neuronal vulnerability, as an effect of
 132 ethanol pre-exposure, is maintained over the 20-h period of reoxygenation following
 133 OGD (33.4 \pm 2.3% cell death, n = 5 for the ethanol-treated neurons, vs. 22.4 \pm 1.1%
 134 cell death, n = 4 for the non-treated neurons, p-value = 0.004).

135 2.3 *Dynamic recording of neuronal death during reoxygenation*

136 Neuronal delayed death was dynamically recorded for 20 h by PI signal to gain
 137 further insight into how ethanol pre-exposure affects neuronal susceptibility to
 138 different levels of metabolic deficits. Figure 3A provides typical examples of such
 139 recordings for each of the conditions used in this study. Maintenance of the primary
 140 neuronal cultures for 20 h in the low-nutrient PI-containing experimental medium
 141 could result in metabolic stress, which induced a low, but constant rate of neuronal
 142 cell death in control cultures. For the first few hours of PI-signal recording, there was
 143 no significant difference between the ethanol-treated and the non-treated neurons. The
 144 sensitising effect of ethanol pretreatment became manifest only after 10-11 h in
 145 control cultures. In case of the more demanding metabolic stress induced by OGD, the
 146 higher death vulnerability of the ethanol-treated neurons was clearly manifest from
 147 the beginning of reoxygenation period (Fig. 3A). These results suggest that neurons
 148 from ethanol-exposed pups have an additional susceptibility to hypoxic-ischemic

challenge that is separate from the toxic effect of ethanol alone. Figures 3B and 3C illustrate these differences across the experimental set using an hourly rate of neuronal cell death as the measured parameter. Figure 3B shows the sensitising effect of ethanol pretreatment becoming manifest only in the latter part of the experimental protocol in control cultures (p-value < 0.001, n = 6 ethanol-treated control group and n = 4 non-treated control group).

After OGD exposure, ethanol-treated cultures showed a significantly different vulnerability in comparison to control cultures (p-value < 0.001, n = 4 for non-treated group and n = 5 for ethanol-treated group). OGD induced extensive damage in the ethanol group during early reoxygenation, as shown by hourly cell death rate $2.9 \pm 0.4\%$ /hour compared to ethanol non-treated cultures $0.73 \pm 0.17\%$ /hour (Fig. 3C). Given the significant death of the ethanol-treated neurons during the first part of the dynamic recording, hourly cell death rate in late reoxygenation was higher in the control group (Fig. 3C), but overall OGD-induced cell death was still higher in the ethanol group at the end of reoxygenation ($66.5 \pm 2.9\%$ vs. $41.5 \pm 2.1\%$) (Fig. 3A).

2.4 Microarray gene expression in control and ethanol-exposed mouse embryos

In the attempt to understand the molecular mechanism which renders ethanol-treated neurons more vulnerable to metabolic stresses, we analyzed gene expression data available on a public-domain microarray dataset (GSE9545 from Gene Expression Omnibus Database), which provides the nearest model example to our experimental model. In this experiment whole embryo mouse cultures were performed on four control embryos and four ethanol-treated ones, the latter characterized by a phenotype of open neural tubes (Wang et al., 2008). Transcriptomic studies suggest that teratogenic effects observed in whole embryo cultures are relevant to previously

173 identified mechanisms of toxicity *in vivo* (Genschow et al., 2002; Luijten et al., 2010;
174 Zhou et al., 2011).

175 Given our *in vitro* observations suggesting a metabolic deficiency induced by ethanol
176 exposure of the offspring, we assessed the effect of ethanol exposure on whole
177 embryo changes in gene expression in various sets of relevant genes. Thus, informed
178 by our *in vitro* data we used an additional model as a probe for the potential changes.
179 Validation of the observed vulnerability on a molecular level in the whole embryo
180 cultures model would provide an important link to the *in vivo* developmental toxicity
181 (Robinson et al., 2012a).

182 A widely used systems biology technique to highlight biological processes is gene
183 category over-representation analysis (Park et al., 2014). To perform this analysis
184 genes are grouped into categories by a common biological property and then tested to
185 find categories that are over-represented. To this end gene ontology (GO) pathways
186 (Ashburner et al., 2000) that are affected by exposure to ethanol were investigated.
187 After removing genes which were not reliably detected, we ranked and clustered
188 16,117 genes according to the expression fold change between the ethanol-exposed
189 and control embryos. Genes clustered in 161 GO categories after correcting for
190 multiple testing by the stringent method of family-wise error rate (FWER < 0.01)
191 (Krzywinski and Altman, 2014). Categories that could be relevant to the higher
192 susceptibility towards metabolic stressors secondary to ethanol exposure of the
193 embryo were further analyzed (Table 1).

194 To identify genes that might be responsible for the observed neuronal susceptibility
195 towards metabolic stressors of ethanol-exposed embryos we first screened the GO
196 category “oxidation-reduction process” (GO:0055114, p-value = 8.80e-08,

FWER < 1.0e-04). This category had an enrichment in genes that were low ranked according to the fold change between the ethanol-exposed group and control, which is translated in a higher number of down-regulated genes than expected by chance. *Dhcr24* (gene coding 24-dehydrocholesterol reductase, p-value = 0.006, fold change = 1.13) and *Cp* (gene coding ceruloplasmin, p-value < 0.001, fold change = 0.71) were the most significantly up and down-regulated, respectively (Table 2).

The category “mitochondrial respiratory chain” (GO:0005746, p-value = 6.27e-06, FWER = 0.003) was enriched in genes that were low ranked, but among the 45 genes in the node none fulfilled the fold change criterion of up- / down-regulation by at least 10%.

Genes that might be responsible for the developmental effects of ethanol on embryos were revealed by focusing on two GO biological processes: “*in utero* embryonic development” (p-value = 2.04e-06, FWER = 0.003) and “nervous system development (p-value = 5.5e-08, FWER = 0.0001)”. This resulted in 4 significantly up-regulated genes involved in embryonic development (GO:0001701) (Table 2), of which *Nrk* (gene coding Nik-related protein kinase, p-value = 0.02, fold change = 1.18) was the most significant. Additionally, 7 genes clustering in this category (Table 2) were significantly down-regulated, with *Slit2* (gene coding Slit homolog 2 protein, p-value = 0.002, fold change = 0.89) most significant. Significantly differentially expressed genes, which clustered in the nervous system development category (GO:0007399) are presented in Table 2, with 19 up-regulated and 21 down-regulated representatives. Of these the most significant up- / down-regulated ones were respectively: *Pitx1* (gene coding paired-like homeodomain

transcription factor 1, p-value = 0.003, fold change = 1.13) and *Slit2*, which clustered in both the previous and this category.

2.5 Gene expression quantification on cerebellar granule neurons cultures from ethanol-exposed and control rat offsprings

To verify which genes could be responsible for the higher vulnerability of ethanol-treated neurons to metabolic stresses, we quantified gene expression levels for candidates obtained from the microarray analysis. The overlap of differentially expressed genes on the CGCs model and whole embryo cultures lends further support to the validity of the identified candidate genes.

We validated five genes as possible candidates: *Dhcr24*, *Bdnf*, *Mapk8*, *Bax*, and *Slc2a4* (Fig. 4). It is common that given the different techniques, qPCR and microarray measurements show different fold changes of the genes, even when the same samples are measured (Lussier et al., 2015). In the case of *Dhcr24* the fold change between the ethanol group and the control is 23 ($\Delta\Delta C_T = 4.55$), while the microarray data showed an increase of only 1.13 fold. *Bdnf* shows a marked up-regulation of 32 fold ($\Delta\Delta C_T = 5.04$), while in the microarray data the gene is found to be down-regulated in the ethanol group (fold change = 0.81, Table 2).

Although the last three genes did not show differential expression in the whole mouse embryo culture model, the rationelle for their measurement was the involvement in the GO categories which showed disruption and may be relevant for the ethanol-induced increased susceptibility towards metabolic stressors (Table 1). While MAPK8 interacting proteins 1 and 2 showed an up regulation after ethanol exposure (Table 2, GO:0032872), *Mapk8* showed no significant regulation (fold change = 1.04). Our measurements revealed a 7.1 fold up-regulation of *Mapk8* in the

245 ethanol group ($\Delta\Delta C_T = 2.82$). *Bax* and *Slc2a4* were also up-regulated in the ethanol
246 group samples to 7.95 fold and 41 fold, respectively ($\Delta\Delta C_{T_{Bax}} = 2.99$ and
247 $\Delta\Delta C_{T_{Slc2a4}} = 5.39$).

248 Genes involved in the oxidative stress response (*Cp*, *Snca*, *Gss*) failed to reach
249 significance in the qPCR measurements.

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3 Discussion

Our study indicates that ethanol exposure during nervous system development results in a significantly higher neuronal vulnerability to metabolically demanding conditions, either under chronic conditions, such as maintenance in a low nutrient medium, or in more acute conditions, such as OGD, which is the *in vitro* equivalent of hypoxia/ischemia.

In their review, Bosco and Diaz hypothesised that ethanol-induced fetal growth retardation occurs most likely as a result of hypoxia and increased oxidative/nitrative stress, which interfere with cellular processes that require oxygen in order to function adequately, such as placental transport (Bosco and Diaz, 2012). Although tested only on one type of cells, the *in vitro* CGCs results support this hypothesis since ethanol exposure during brain growth spurt aggravates the cellular damage induced by a hypoxic/ischemic injury (Figs. 2 and 3).

To validate the ethanol-induced vulnerability in an additional model, but also to understand the mechanisms that underlie the ethanol-sensitizing effect to both chronic and acute metabolic challenges, we performed gene expression data analysis on a publicly available microarray dataset from whole embryo cell cultures. Whole embryo cell cultures show gene expression patterns very similar, over time, to *in utero* embryos; and, in the case of rat, cultures are matching to a great extent the gene expression profile in human embryos undergoing neurulation and early embryogenesis (Robinson et al., 2012b). Therefore, given the high *in vivo* translation potential of whole embryo cell cultures (Genschow et al., 2002), the results can benefit of better support for a possible *in vivo* extrapolation. However, whole embryos display tissue heterogeneity, which may mask some changes in specific tissues or cells (Zhou et al., 2011). Hence, we validated some of the candidate genes on the *in*

276 *vitro* model of CGCs cultures originating from offspring exposed to ethanol during
 277 cerebellar development.

278 We assessed expression patterns of genes involved in pathways correlated with a
 279 higher metabolic vulnerability. Mitochondrial dysfunction plays a key role in hypoxic
 280 neuronal injury and could therefore be a determining factor in the CGCs' damage
 281 caused by ethanol preexposure. Upon inquiry of the "mitochondrial respiratory chain"
 282 GO category, there was a significant enrichment with down-regulated genes, but
 283 given the strict cutoffs set for candidate genes, none of the genes in this cluster
 284 reached the threshold for significance. Since a strict cut-off to limit false-positive
 285 results leads to an increase of the number of false negative results (Kowalchuk and
 286 Keselman, 2001), and also because oxidative stress has been recently described as an
 287 important factor in the pathophysiology of alcohol-induced impairment (Joya et al.,
 288 2014), we further investigated other related pathways.

289 A close inspection of the GO category "oxidation-reduction process" revealed an
 290 ethanol-induced up-regulation of *Dhcr24* shown to exert a neuroprotective effect
 291 against reactive oxygen species resulted from endoplasmic reticulum stress (Lu et al.,
 292 2014). The down-regulation of *Cp*, an important antioxidant molecule, is in
 293 accordance to previous studies on hippocampi after chronic ethanol exposure (Saito et
 294 al., 2002). Another down-regulated gene of the pathway is *Snca*, a synaptic molecule
 295 involved in neurodegenerative disorders and an oxidative stress protector of neuronal
 296 cells (Hashimoto et al., 2002). While *Dhcr24* was verified by qPCR on the CGCs
 297 model, *Cp* and *Snca* failed to reach significance. Still, we cannot exclude that on the
 298 whole embryo level oxidative stress plays an important role in the ethanol-induced
 299 pathology. However, the proapoptotic mitochondrial-membrane associated *Bax*
 300 showed an elevated expression in the ethanol group on CGCs. It has recently been

shown that ethanol exposure of rats on postnatal day 4 leads to an increased activation of BAX (Heaton et al., 2015), which together with high expression levels of the gene, could lead to apoptosis. Nonetheless, under basal conditions we could not detect morphologically higher apoptotic levels in the ethanol group (Figures 1 and 3A). Overexpression of *Dhcr24* was shown to inhibit apoptotic cell signaling, hence it seems reasonable to assume that the observed upregulation of *Dhcr24* is a counterbalance that prevents the commitment on the activated apoptotic pathway in CGCs.

Additionally, it is notable that *Bdnf*, a gene that appears down-regulated following ethanol exposure of embryos, can have protective effects on cerebellar granule neurons under low glucose conditions (Vakili Zahir et al., 2012). *Bdnf* was shown to prevent JNK and p38 activation in stress conditions and thus increase cell viability. The CGCs *in vitro* expression data confirm the overexpression of *Mapk8 (Jnk1)*, which is known to promote apoptosis (Dhanasekaran and Reddy, 2008). Conversely, *Bdnf* is up-regulated after ethanol exposure in the CGCs model, unlike on whole embryo cultures. It seems likely that up-regulation of both genes maintains a balance in the basal viability and we hence observe a higher vulnerability only under challenging conditions.

We show that *Slc2a4*, the transcript coding for the insulin-sensitive glucose transporter GLUT4, is up-regulated after ethanol exposure in CGCs. GLUT4 was described to be present in significant amounts in CGCs and was shown to be up-regulated in the CGCs of a diabetic, hyperinsulinemic mouse model (Vannucci et al., 1998). CGCs showed an opposite expression profile in the diabetic mice when compared to periferic tissues in which *GLUT4* transcript was decreased. Additionally, prenatal alcohol exposure induces impaired glucose tolerance (Chen et al., 1996).

326 Thus, *Slc2a4* might be a key candidate to explain the impaired cerebellar glucose
 327 metabolism and high susceptibility to *in vitro* hypoxia and hypoglycemia in cultured
 328 CGCs from prenatally ethanol-exposed rats.

329 *Adm*, a shared down-regulated gene between “embryonic and nervous system
 330 development” GO categories, was shown to lead to lower resistance to hypobaric
 331 hypoxia in mice that were *Adm* conditional knockouts in the central nervous system
 332 (Fernandez et al., 2008). Moreover evidence points towards an involvement of this
 333 gene in placentation and regulation of fetal perfusion (Wilson et al., 2004), which
 334 together with the known ethanol cytotoxic effects on trophoblast cells (Clave et al.,
 335 2014) may support an altered placental function in ethanol drinking dams. Although
 336 not significantly disrupted in CGCs, the expression of the *Adm* gene seems to be more
 337 relevant on an entire organism level, such that mild impairment of the placental
 338 function could result in decreased neuronal viability.

339 Taken together ethanol might confer a higher risk towards hypoxic/ischemic events,
 340 which can lead to growth retardation as suggested by Bosco and Diaz (Bosco and
 341 Diaz, 2012) given the confirmed predisposition towards hypoxia and glucose
 342 deprivation in the neurons. Furthermore, in CGCs, survival was reduced, with a
 343 certain lag time, even under less severe metabolic conditions, such as the *in vitro*
 344 maintenance of neurons in an artificial environment, with a relative reduction in the
 345 supply of nutrients (Fig. 3). We show that in our experimental model genes involved
 346 in apoptosis have a higher expression level after ethanol treatment. However,
 347 compensatory mechanisms involving neuroprotective genes, which we show to be up-
 348 regulated, are probably responsible for the apparent similar viability between the
 349 ethanol-exposed and control neurons.

350 In sum, the present results suggest an ethanol-induced reduction of the cellular
351 adaptation to stress, which was verified in both, the *in vitro* CGCs cultures and on a
352 molecular level in whole embryo cultures. The gene profiles and the observed pattern
353 of ethanol-treated neurons impairment should both together contribute to the
354 generation of *in vivo* studies concerning secondary prevention of brain damage, such
355 as avoiding additional mild hypoxic events or metabolic stressful circumstances in the
356 newborn.

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4 Experimental Procedure

4.1 Animals

Sixteen pregnant Wistar rats and thirty-one of their litters from the breeding colony at Carol Davila University of Medicine and Pharmacy were used in this study. All animal procedures were carried out with the approval of the local ethics committee for animal research of Carol Davila University of Medicine and Pharmacy (Bucharest, Romania), and in accordance with the European Communities Council Directive 86/609/EEC on the protection of animals used for scientific purposes. All efforts were made to minimize the number of animals used and their suffering.

4.2 Ethanol treatment

Pregnant rats were randomly assigned on the day of confirming pregnancy, to either an ethanol group or a non-treated group and housed separately thereafter. Both groups had free access to food and liquids, and the ethanol group dams were given ethanol 20% v/v in the drinking water to induce ethanol exposure damage to the litter (Snyder et al., 1992). To validate the level of ethanol exposure, blood alcohol levels (BAL) were randomly measured during the entire setup time frame using an enzymatic, UV method (Dialab, Austria). This type of exposure resulted in maternal BAL of 112.7 ± 19.3 mg/dL ($n = 6$) (data represent mean value \pm SEM). Nutrition and drinking patterns were daily monitored for both groups, and no nutritional deficits were observed. Mean block-food ingestion did not significantly differ between ethanol treated and non-treated group, with an average calorie intake of 269.1 ± 6.8 kcal/kg body weight/day (data represent mean value \pm SEM). Liquids consumption in the non-treated group was 129.2 ± 5.3 ml/kg body weight/day. The fluid ingestion in the ethanol treated group was 139.6 ± 9.5 ml/kg body weight/day, of

which an average of 22.0 ± 1.6 g ethanol/kg body weight/day. The body weight did not differ significantly between the two groups at different pregnancy stages.

To mimic ethanol exposure during the third trimester of pregnancy in humans, full-term litters, known to correspond developmentally to the end of the second trimester in humans, were further exposed to ethanol through lactation until postnatal day 5, as the dams continued to receive ethanol 20% v/v in the drinking water (Olney et al., 2000). BAL was monitored during this period, by random serum measurements, and reached values of 109.7 ± 43.9 mg/dl in pups ($n = 4$). As ethanol exposure through breastfeeding might not be sufficient to induce a similar to human third-trimester exposure causing cerebellar dysfunction (Cebolla et al., 2009), postnatal day 5 pups were exposed to a “binge-like” pattern of ethanol consumption, common in women who drink during pregnancy (Maier et al., 1997). This ethanol acute exposure was mimicked by a 3-hour vapor inhalation (Heaton et al., 2000b), resulting in a BAL of 461.5 ± 165.8 mg/dl ($n = 4$) in pups, a concentration comparable to the high levels seen in previous human and animal studies (Tran et al., 2005). The chronic and acute combinatorial model of ethanol exposure corresponds to the behavioral pattern of steady drinkers (Epstein et al., 1995). Cerebella did not significantly differ in either morphology or weight compared to unexposed pups.

4.3 Cerebellar granule neurone cultures and oxygen-glucose deprivation exposure

The exposure model was further transferred into an *in vitro* setup allowing a better assessment of the deleterious effects which ethanol exerts on cerebellar granule neurons. CGCs cultures are widely used for the *in vitro* study of neuronal ischemia (Kalda et al., 1998) or ethanol neurotoxicity (Heaton et al., 2000a; Luo, 2012) since they provide a homogenous population of glutamatergic neurons in which experimental conditions can be precisely controlled (Contestabile, 2002). Primary

407 cultures of cerebellar granule neurons were obtained as previously described (Toescu,
408 1999) immediately after the acute ethanol exposure or a sham air exposure, for
409 ethanol and non-treated pups, respectively. Briefly, the dissociated cell suspensions
410 from cerebella of 5-day-old pups were plated at a density of 200,000 cells/well into
411 96-well plates (Nunc) coated with poly-D-lysine (Sigma-Aldrich) in complete BME
412 culture medium (Sigma-Aldrich) containing 2 mM L-glutamine (HyClone), 32 mM
413 glucose, 10% heat-inactivated horse serum (Sigma-Aldrich), antibiotic-antimycotic
414 (GIBCO/Invitrogen) and 25 mM KCl, to promote CGCs viability in culture (Gallo et
415 al., 1987). Cytosine-arabioside (Sigma-Aldrich, 10 μ M) was added after 24 h to stop
416 the glial cells proliferation. There were no apparent differences between the cultures
417 generated from ethanol-treated group and the cultures from the non-treated group, in
418 regard to morphology or number of viable neurons. Cultures were grown in a
419 humidified incubator at 37°C and 5% CO₂ for 7 days until they reached a maturation
420 level that allowed evaluating different experimental conditions. The percentage of
421 glial cells was no more than 1% as assessed by glial fibrillary acidic protein and β -
422 tubulin immunostaining. The cultures were grown in ethanol-free solutions to
423 promote similar adaptation to *in vitro* state for both groups. Control condition and
424 OGD which mimics ischemia *in vitro* (Goldberg et al., 1986), were carried out as
425 previously described (Ceanga et al., 2010), by shifting cultures in a serum-free
426 experimental medium (EM) with or without glucose (EM+G, EM-G, containing in
427 mM: 120 NaCl, 25 KCl, 0.62 MgSO₄, 1.8 CaCl₂, 10 HEPES, \pm 11.1 glucose, pH 7.4).
428 Briefly, OGD was initiated by washing cultures with EM-G to remove glucose before
429 adding deoxygenated EM-G. Then, cultures were immediately placed into a
430 humidified hypoxia chamber (Billups-Rothenberg Inc., Del Mar, CA) which was
431 flushed with 100% N₂ for 10 min, sealed, and placed into an incubator at 37°C for 3 h,

an OGD exposure time that we previously found to induce neuronal damage (Zagrean A.M., 2007-Personal Communication). Reoxygenation was induced by replacing EM-G with normoxic EM+G. Control cultures went through identical steps except they were kept in normoxic EM+G in a 5% CO₂ incubator at 37°C (control condition).

4.4 Experimental groups

Four experimental groups were defined to evaluate the neuronal vulnerability to a metabolic stress, considering both the *in vivo* ethanol treatment and the *in vitro* exposure of CGCs cultures to OGD or control conditions: two ethanol-treated groups, an ethanol OGD group and an ethanol control group, and two non-treated groups, a non-treated OGD group and a non-treated control group.

4.5 Assessment of cellular viability

4.5.1. Microscopic examination

Morphology and cell maturation were assessed in phase-contrast microscopy with a Zeiss Axiovert25 inverted microscope at 400× magnification during the cultures' growth period and no morphological difference between ethanol-exposed neurons and neurons from non-ethanol treated pups were observed. Cellular morphology was also assessed immediately after OGD or control conditions. The wells containing disrupted cultures were discarded. The cellular damage induced by ethanol pretreatment and OGD was further morphologically assessed in phase-contrast microscopy at the end of reoxygenation period.

4.5.2. PI fluorometry

The rate of delayed cell death was monitored for the next 20 hours after control and OGD conditions by use of a vital dye, PI (Sattler et al., 1997), which becomes fluorescent upon binding the DNA of membrane-compromised cells (Vornov et al.,

1995). Cells were washed once with 200 μ l EM+G immediately after OGD or control conditions, then 100 μ l PI solution (50 μ g/ml in EM+G) was added in each well. The initial level of PI fluorescence in a sequence of five readings at 60 seconds interval was read in a multimode detector (DTX880, Beckman Coulter) set in fluorescent mode with an excitation wavelength of 535 nm and an emission wavelength of 625 nm. Dynamic PI measurements were initiated at every 15 minutes for 20 hours of reoxygenation at 37°C. At the end of reoxygenation time, the PI solution was exchanged with 25 μ l ethanol (100%)/well to induce maximal death. After ethanol evaporation the PI solution was added back and the maximal signal (corresponding to the total number of cells) was measured in a sequence of 5 readings at 60 second intervals.

4.6 *Microarray gene expression analysis*

Microarray expression data was obtained from the public database Gene Expression Omnibus under the accession number GSE9545. We analyzed the dataset that measured the global gene expression profiles in whole mouse embryo cultures, comparing control with alcohol treated embryos that had a clear phenotype which consisted in open neural tubes. A full description of the experimental ethanol model is available in the study of Wang et. al (Wang et al., 2008). Microarray expression was calculated using the *affy* (Gautier et al., 2004) and *gcrma* (Wu et al., 2004) of the *Bioconductor* (Gentleman et al., 2004) extensions to the R statistical programming environment (<http://www.R-project.org>). Genes that were not reliably detected in at least one of the two conditions were removed from further analysis. To identify metabolic pathways influenced by ethanol exposure genes were clustered in gene ontology categories (Ashburner et al., 2000) using *FUNC* package (Prufer et al., 2007) with a Wilcoxon ranking test according to the fold change of gene expression.

Family-wise error rate (< 0.01) was used to correct for multiple testing hypothesis (Krzywinski and Altman, 2014). On the gene expression level a two sample *t*-test was used for statistical analysis. The MicroArray Quality Control (MAQC) project has shown that results of typical statistical differential expression tests with p-value as significance threshold need to be filtered and sorted by effect strength (fold-change) to attain robust comparisons across platforms and sites (Consortium et al., 2006). Hence, genes were defined as candidates if they clustered in a significant GO category, had a p-value < 0.05 and a fold change between the ethanol-treated and control group either lower than 0.9, or higher than 1.1. Significance level of genes in the analyzed GO categories was established according to p-value and fold change between the ethanol group and control.

4.7 Cerebellar granule neurons cDNA preparation and quantification by qPCR

CGCs originating from rat pups exposed to ethanol, or under control conditions were obtained as described above. Offsprings originated from two dams for each group, cerebella were collected, three and four cell cultures were made for the control and ethanol-group, respectively. Total RNA was isolated using 500 μ l TRI REAGENT™ (Sigma Aldrich) according to the manufacturer's instructions. 550 ng of RNA were reverse transcribed (Superscript, Invitrogen™) with oligo(dT) primer in a total reaction volume of 20 μ l. 1 μ l of cDNA was further subjected to real-time PCR using Platinum-SYBR Green qPCR Supermix (Invitrogen), forward and reverse primers (0.9 μ M), and ROX (100 nM, 5-carboxy-X-rhodamine, passive reference dye). Primers were designed with the Primer3 software for the following genes: *Cp* (forward primer: 5'-CATGTGGATGCTCCAAAAGA-3', reverse primer: 5'-GGTTCCGAGCAGAAGGTTTT-3'), *Dhcr24* (forward primer: 5'-GCTCTCCCTCATCTTCGACA-3', reverse primer: 5'-

506 TGAGACAGTGAGCCATCCAG-3', *Adm* (forward primer: 5'-
 507 CTCGACACTTCCTCGCAGT-3', reverse primer: 5'-
 508 AGACGTGCTCTGCTTGTCTCCT-3'), *Bdnf* (forward primer: 5'-
 509 AGGAGCGTGACAACAATGTG-3', *Snca* (forward primer: 5'-
 510 AGAAAACCAAGCAGGGTGTG-3', reverse primer: 5'-
 511 CCCTCCACTGTCTTCTGAGC-3'), reverse primer: 5'-
 512 CGTGGACGTTTGCTTCTTTC-3'), *Mapk8* (forward primer: 5'-
 513 CGGAGATTCTACATTCACAGTCC-3', reverse primer: 5'-
 514 CGCTTAGCATGGGTCTGATT-3'), *Bax* (forward primer: 5'-
 515 GCTGGACACTGGACTTCCTC-3', reverse primer: 5'-
 516 CTCAGCCCATCTTCTTCCAG-3'), *Slc2a4* (forward primer: 5'-
 517 GGCCGGGACACTATACCCTA-3', reverse primer: 5'-
 518 GCCAAGCACAGCTGAGAATA-3'), *Gss* (forward primer: 5'-
 519 AGGGGGTGTGCTGAGGT-3', reverse primer: 5'-
 520 CTGGCTGACAGCATCTACCA-3'), and *B2m* (forward primer: 5'-
 521 ACATCCTGGCTCACACTGAA-3', reverse primer: 5'-
 522 CCGGATCTGGAGTTAACTGG-3'). PCR was performed in an MX 3000P
 523 instrument (Stratagene, La Jolla, CA) using the following protocol: 5 min 50°C, 2 min
 524 95°C, and 40 cycles of 15 s 95°C, 30 s 60°C. A product melting curve was recorded
 525 to confirm the presence of a single amplicon. The correct amplicon size was
 526 confirmed by agarose gel electrophoresis. Threshold (C_T) values were set within the
 527 exponential phase of the PCR. *B2m* shows constant level of expression in both
 528 ethanol-treated and control cell cultures (C_T values of 17.7 ± 0.5 and 17.9 ± 0.2 ,
 529 respectively), which supports its use as housekeeping gene (Butte et al., 2001). The
 530 housekeeping gene *B2m* (β 2-microglobulin) was used for normalization

531 $\Delta C_T (C_{T(\text{gene})} - C_{T(B2m)})$ (Livak and Schmittgen, 2001). The relative expression levels
 532 are given as the difference between the ΔC_T corresponding to the non-treated and
 533 ethanol-treated groups, respectively, $(\Delta \Delta C_{T(\text{gene})} = \Delta C_{T(\text{gene Non-treated Group})} -$
 534 $\Delta C_{T(\text{gene Ethanol Group})})$. Gene regulation ratios between the ethanol and control groups
 535 are given as $2^{\Delta \Delta C_T}$ values (Livak and Schmittgen, 2001). Gene regulation was
 536 statistically evaluated by subjecting the ΔC_T values to a two-sided, unpaired Student's
 537 *t*-test.

538 4.8 Statistical analysis for CGCs cultures viability experiments

539 For each group, the experiments were performed at least 4 times, on independent
 540 CGCs cultures from litters of different dams, with multiple wells for each condition.
 541 Statistical analysis was performed considering the different litters as biological
 542 replicates, while corresponding number of culture wells were considered technical
 543 replicates. To account for both technical and biological variance we used a standard
 544 equation for error propagation, as described by Taylor:

545 $SD = \sqrt{SD_{\text{biological replicates}}^2 + SD_{\text{technical replicates}}^2}$ (Taylor, 1997). Numerical results are given
 546 as mean \pm SEM.

547 To analyze whether cell death was influenced by time or assessment conditions, a
 548 multiple regression model was run. No interaction between general predictors was
 549 taken into account, as theory suggests there should be none. Into this we included
 550 conditions and time (covariate) as the two predictors. Prior to running the model we
 551 checked covariate and cell death for having approximately simetrical distributions
 552 (which was the case), and z-transformed covariate to a mean of zero and a standard
 553 deviation of one to achieve easier interpretable coefficients (Forstmeier and
 554 Schielzeth, 2011). We checked model diagnostics like distribution of residuals,

555 Cook's distance and dfbetas and none of these indicated outliers, or obvious
556 deviations from the assumptions of normality and homogeneity of residuals. The
557 model and most diagnostics were run using functions available in R (Team, 2011).
558 Generalized Variance Inflation Factors were derived using the function `vif` of the R
559 package `car` (Weisberg, 2011). Overall the two parameters used for analysis:
560 "assessment conditions" and "time", both influenced cell death at a significant level
561 (comparison of full to the null model results in $F_{3,319} = 1163$, $p < 0.001$). The cell
562 death increased in time (estimate = 9.9613, SE = 0.2425, $t_{319} = 41.079$). Cell death
563 was also influenced by the assessment conditions as shown by comparing the full
564 model with a reduced one not comprising exposure conditions revealed and resulting
565 in an $F_{3,319} = 987.67$, and $p < 0.001$). This validated the data without running pair wise
566 comparisons and allowed for pair wise post-hoc comparisons to analyze the impact on
567 cell survival between different conditions. A value of $p < 0.05$ was considered
568 statistically significant.
569

570 **Conflict of interest statement**

571 The authors declare that they have no competing interests.

572 **Authors contributions**

573 DLD: Participated in the design of the research, experimental procedures, data
574 analysis, microarray gene expression analysis, and manuscript writing.

575 AS: Participated in the design of the research, experimental procedures, and data
576 analysis.

577 MC: Participated in data analysis.

578 LZ: Participated in manuscript writing.

579 TS: Participated in manuscript writing and qPCR experiments design.

580 ECT: Participated in data analysis and manuscript writing.

581 AMZ: Participated in the design of the research, experimental procedures, data
582 analysis, and manuscript writing.

583 All authors have approved the final article manuscript.

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592

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Figure legends:

Figure 1. Microscopy images of CGCs cultures originating from ethanol-treated

or non-treated rat pups. A. Phase-contrast microscopy of CGCs cultures on *in vitro*

day 7 before exposure to OGD and/or normoxic low nutrient medium used for control

shows similar morphology in the ethanol-treated and non-treated groups. **B.** Phase-

contrast microscopy (upper pannel) and fluorescent (bottom pannel) images taken on

the same field from non-treated and ethanol treated CGCs stained with propidium

iodide, after 20 hours of reoxygenation following OGD or control conditions.

Microphotographs were taken with a Zeiss Axiovert25 inverted microscope at 400x

magnification. Scale bar represents 10 μ m.

Figure 2. Cell death of ethanol-treated and non-treated cerebellar granule

neurons exposed to OGD. A. At the beginning of reoxygenation cell death was

found significantly increased in the ethanol-treated group exposed to OGD. Cell death

was assessed by propidium iodide fluorescence. **B.** The effect of OGD on ethanol-

treated and non-treated cultures after 20 hours of reoxygenation is expressed as % cell

death difference between OGD and control cultures. At this time point, OGD-induced

cell death remained significantly increased in the ethanol group, comparing with the

non-treated group. Error bars represent SEM, $n \geq 4$ cell cultures from unrelated pups.

Figure 3. Cell death over 20 hours of reoxygenation in ethanol-exposed and non-

treated cerebellar granule neurons subjected to OGD. A. OGD-induced higher

cell death rates in ethanol-exposed neurons in comparison to non-treated ones. Under

control conditions the difference between ethanol-exposed cells and non-treated ones

became manifest after 10 hours of reoxygenation. Cell death was assessed every

15 minutes for 20 hours by propidium iodide fluorescence. **B.** In control cultures,

hourly cell death rate calculated during early (2-7 h) and late (12-17 h) reoxygenation,

showed that the sensitising effect of ethanol pretreatment becomes manifest only during the late reoxygenation. **C.** OGD effect on hourly cell death rate, calculated as difference between OGD and control cultures, was significantly higher during early reoxygenation in ethanol-exposed neurons compared to non-treated ones. Due to the extensive damage during early reoxygenation in ethanol group, the hourly cell death rate during the late reoxygenation period became higher in non-treated cultures. Error bars represent SEM, $n \geq 4$ CGCs cell cultures from unrelated pups.

Figure 4. qPCR measurement of genes hypothesized to be influenced by prenatal alcohol exposure. Five genes are significantly up-regulated in the ethanol-exposed neurons compared to the non-treated ones. The measured genes are involved in the GO categories shown to be disrupted on a microarray dataset from whole embryo cell cultures after ethanol exposure (Tables 1 and 2). $\beta 2$ -microglobulin (*B2m*) expression levels are similar between the ethanol-exposed (17.7 ± 0.5) and non-treated CGCs cultures (17.9 ± 0.2). C_T values for *B2m* were used for normalization $\Delta C_T (C_{T(\text{gene})} - C_{T(B2m)})$. Error bars represent SEM, $n = 3$ and $n = 4$ for CGCs cultures of non-treated and ethanol-treated groups, respectively.

Table 1. Gene Ontology categories relevant for an increased susceptibility towards metabolic stressors observed in ethanol-exposed embryos. GO enrichment was tested using a Wilcoxon rank test from FUNC package, according to expression fold change between ethanol-exposed and control embryos. FWER = family wise error rate. First two nodes are enriched in low ranked genes and the others in high ranked ones.

Root node name	Node name	Node ID	No. of genes in node	raw p-value	FWER
biological process	oxidation-reduction process	GO:0055114	587	8.80E-08	< 1.0E-04
cellular component	mitochondrial respiratory chain	GO:0005746	45	6.27E-06	0.003
biological process	regulation of stress-activated MAPK cascade	GO:0032872	133	3.28E-06	0.005
biological process	in utero embryonic development	GO:0001701	346	2.04E-06	0.003
biological process	nervous system development	GO:0007399	1392	5.50E-08	< 1.0E-04

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Table 2. Differentially expressed genes which clustered in “oxidation-reduction process” GO:0055114, “regulation of stress-activated MAPK cascade” GO:0032872, “*in utero* embryonic development” GO:0001701, and “nervous system development” GO:0007399 categories. p-values were calculated gene-wise using a two sample *t*-test and fold EtOH/Ctr represents the fraction between the mean expression value in the ethanol-exposed versus control embryos.

826 GO:0055114

Gene name	Gene description	p-value	Fold EtOH/Ctr
<i>Dhcr24</i>	24-dehydrocholesterol reductase	0.006	1.13
<i>Fads2</i>	fatty acid desaturase 2	0.018	1.13
<i>Adh1</i>	alcohol dehydrogenase 1 (class I)	0.026	1.12
<i>Gpd1l</i>	glycerol-3-phosphate dehydrogenase 1-like	0.037	1.15
<i>Cp</i>	ceruloplasmin	< 0.001	0.71
<i>Blvrb</i>	biliverdin reductase B (flavin reductase (NADPH))	< 0.001	0.80

	<i>Pnpo</i>	pyridoxine 5'-phosphate oxidase	< 0.001	0.89
	<i>Snca</i>	synuclein, alpha	0.004	0.85
	<i>Bdnf</i>	brain derived neurotrophic factor	0.011	0.81
	<i>Ppp1r3c</i>	protein phosphatase 1, regulatory (inhibitor) subunit 3C	0.017	0.87
	<i>Aifm2</i>	apoptosis-inducing factor, mitochondrion-associated 2	0.028	0.87
	<i>Ppox</i>	protoporphyrinogen oxidase	0.029	0.87
827	GO:0032872			
	Gene name	Gene description	p-value	Fold EtOH/Ctr
	<i>Mapk8ip1</i>	mitogen-activated protein kinase 8 interacting protein 1	0.014	1.18
	<i>Nrk</i>	Nik related kinase	0.021	1.18
	<i>Ephb1</i>	Eph receptor B1	0.026	1.13
	<i>Mapk8ip2</i>	mitogen-activated protein kinase 8 interacting protein 2	0.029	1.12
	<i>Ctgf</i>	connective tissue growth factor	0.013	0.86
	<i>Ncor1</i>	nuclear receptor co-repressor 1	0.016	0.77
	<i>Gadd45a</i>	growth arrest and DNA-damage-inducible 45 alpha	0.030	0.89
	<i>Eda2r</i>	ectodysplasin A2 receptor	0.044	0.85
828	GO:0001701			
	Gene name	Gene description	p-value	Fold EtOH/Ctr
	<i>Nrk</i>	Nik related kinase	0.020	1.18
	<i>Epb4.115</i>	erythrocyte protein band 4.1-like 5	0.020	1.11
	<i>Eif4e2</i>	eukaryotic translation initiation factor 4E member 2	0.020	1.10
	<i>Wnt2</i>	wingless-related MMTV integration site 2	0.042	1.11
	<i>Slit2</i>	slit homolog 2	0.002	0.89
	<i>Cebpb</i>	CCAAT/enhancer binding protein (C/EBP), beta	0.011	0.86
	<i>Maff</i>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	0.011	0.87
	<i>Adm</i>	adrenomedullin	0.021	0.86
	<i>Cyr61</i>	cysteine rich protein 61	0.028	0.89
	<i>Klf1</i>	Kruppel-like factor 1 (erythroid)	0.028	0.79
	<i>Pdgfb</i>	platelet derived growth factor, B polypeptide	0.037	0.89
829	GO:0007399			
	Gene name	Gene description	p-value	Fold EtOH/Ctr
	<i>Pitx1</i>	paired-like homeodomain transcription factor 1	0.003	1.13
	<i>Clmn</i>	calmin	0.005	1.14
	<i>Lrp8</i>	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	0.008	1.16
	<i>Fzd3</i>	frizzled homolog 3 (Drosophila)	0.011	1.14
	<i>Astn1</i>	astrotactin 1	0.023	1.17
	<i>Ephb1</i>	Eph receptor B1	0.026	1.13
	<i>En2</i>	engrailed 2	0.027	1.28
	<i>Apcdd1</i>	adenomatosis polyposis coli down-regulated 1	0.027	1.13

<i>Ncdn</i>	neurochondrin	0.027	1.11
<i>Lpar3</i>	lysophosphatidic acid receptor 3	0.027	1.11
<i>Sall1</i>	sal-like 1 (Drosophila)	0.028	1.12
<i>Mapk8ip2</i>	mitogen-activated protein kinase 8 interacting protein 2	0.029	1.12
<i>Sphk2</i>	sphingosine kinase 2	0.034	1.12
<i>Pax7</i>	paired box gene 7	0.038	1.11
<i>Sox1</i>	SRY-box containing gene 1	0.041	1.16
<i>Pou3f1</i>	POU domain, class 3, transcription factor 1	0.041	1.37
<i>Wnt2</i>	wingless-related MMTV integration site 2	0.042	1.11
<i>Pcsk9</i>	proprotein convertase subtilisin/kexin type 9	0.046	1.12
<i>Prdm6</i>	PR domain containing 6	0.047	1.13
<i>Slit2</i>	slit homolog 2	0.002	0.89
<i>Tenm2</i>	teneurin transmembrane protein 2	0.005	0.83
<i>Limk1</i>	LIM-domain containing, protein kinase	0.006	0.90
<i>Arhgef28</i>	Rho guanine nucleotide exchange factor (GEF) 28	0.008	0.86
<i>Ntf3</i>	neurotrophin 3	0.009	0.88
<i>Cebpb</i>	CCAAT/enhancer binding protein (C/EBP), beta	0.011	0.86
<i>Gfra1</i>	glial cell line derived neurotrophic factor family receptor alpha 1	0.011	0.79
<i>Bdnf</i>	brain derived neurotrophic factor	0.011	0.81
<i>Nrxn1</i>	neurexin I	0.013	0.86
<i>Ncor1</i>	nuclear receptor co-repressor 1	0.016	0.77
<i>Ndr1</i>	N-myc downstream regulated gene 1	0.018	0.77
<i>Trp63</i>	transformation related protein 63	0.019	0.90
<i>Adm</i>	adrenomedullin	0.021	0.86
<i>Dlc1</i>	deleted in liver cancer 1	0.022	0.76
<i>Ndr2</i>	N-myc downstream regulated gene 2	0.025	0.87
<i>Itga1</i>	integrin alpha 1	0.028	0.82
<i>Foxd1</i>	forkhead box D1	0.030	0.88
<i>Etv1</i>	ets variant gene 1	0.030	0.89
<i>Sema3d</i>	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	0.031	0.85
<i>Ankrd1</i>	ankyrin repeat domain 1 (cardiac muscle)	0.038	0.89
<i>Lrrk2</i>	leucine-rich repeat kinase 2	0.040	0.88

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832 **Highlights:**

833 - Fetal ethanol exposure increases neurons' vulnerability towards metabolic stressors

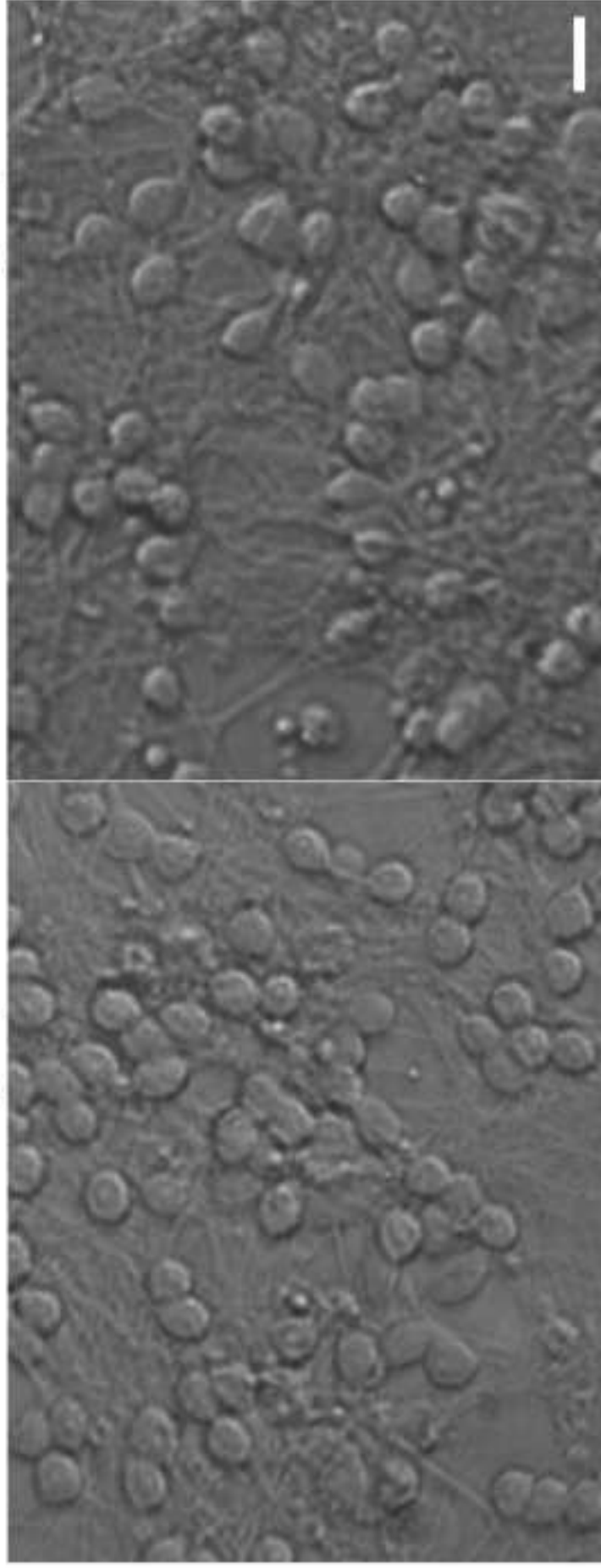
834 - Maternal alcoholism decreases offsprings' neuronal tolerance to hypoxia/ischemia

835 - Ethanol alters expression of genes associated with apoptosis and neuroprotection

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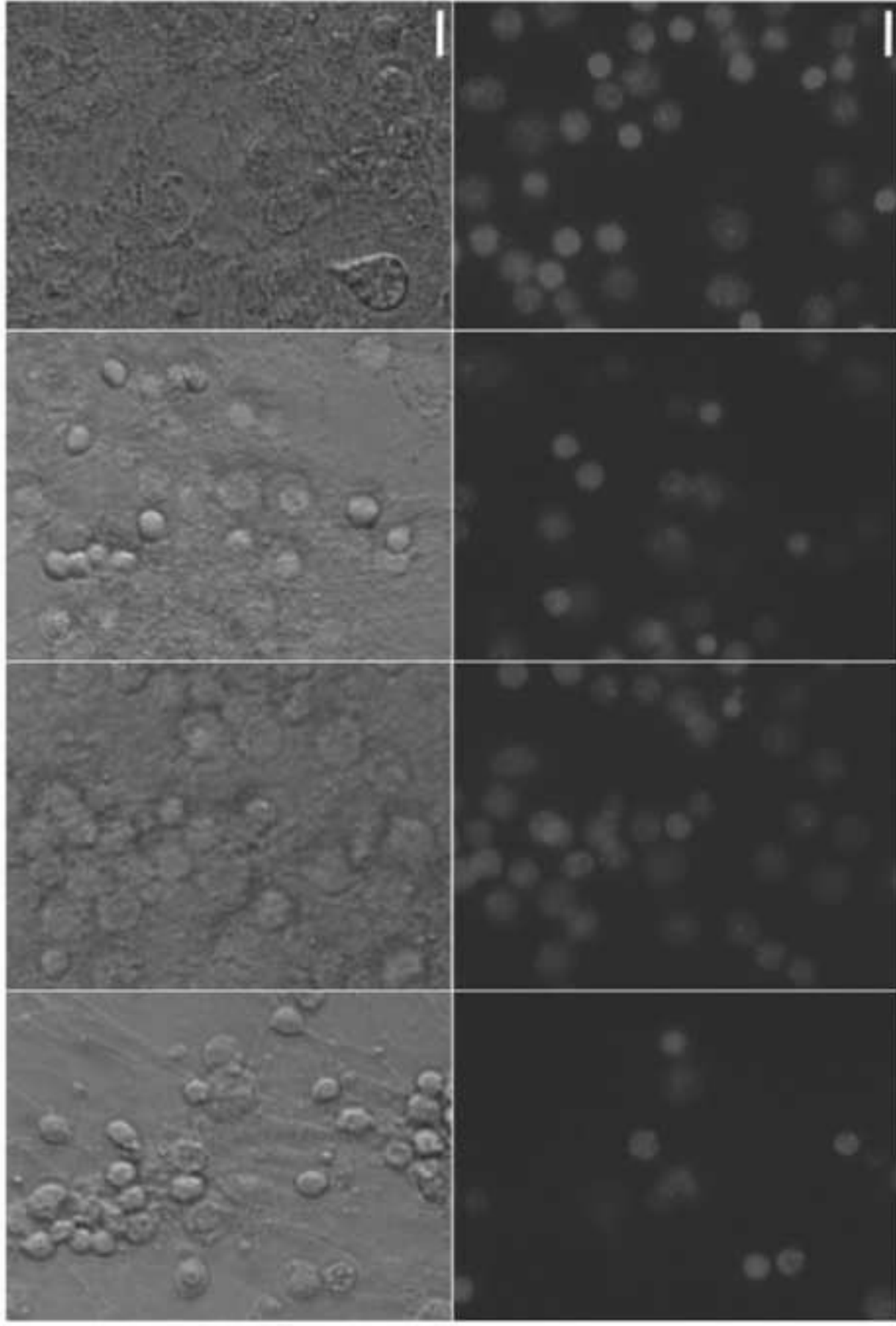
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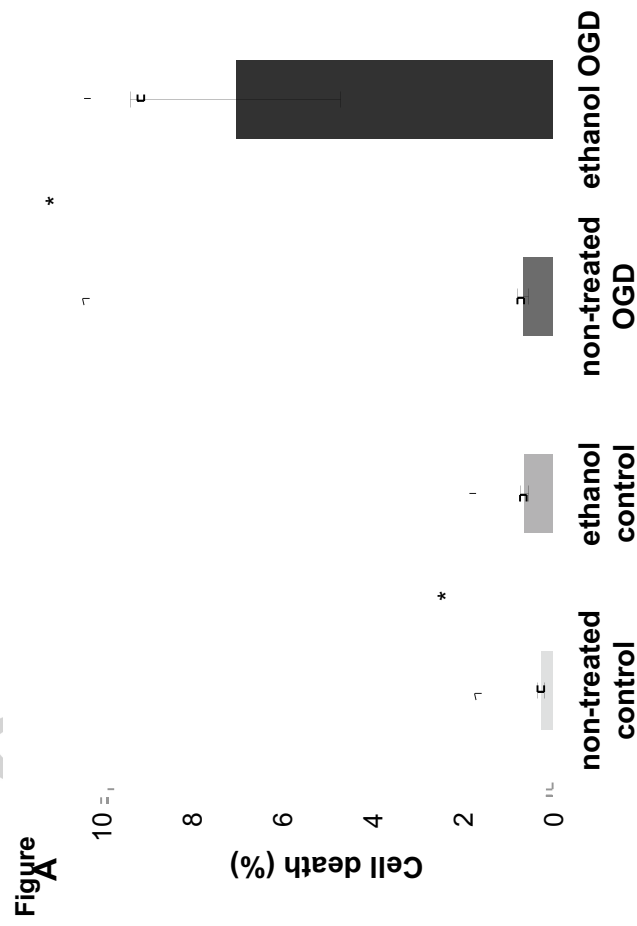
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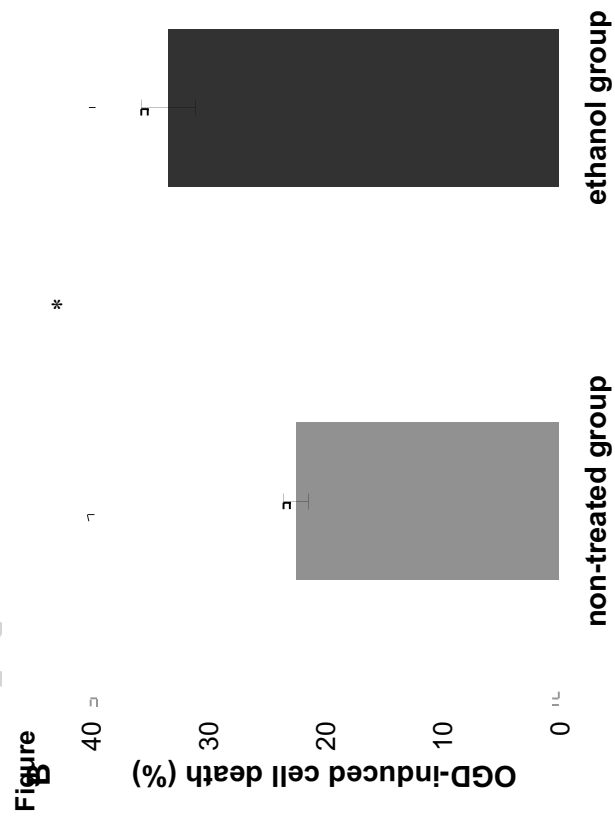
A**non-treated group****ethanol-treated group**

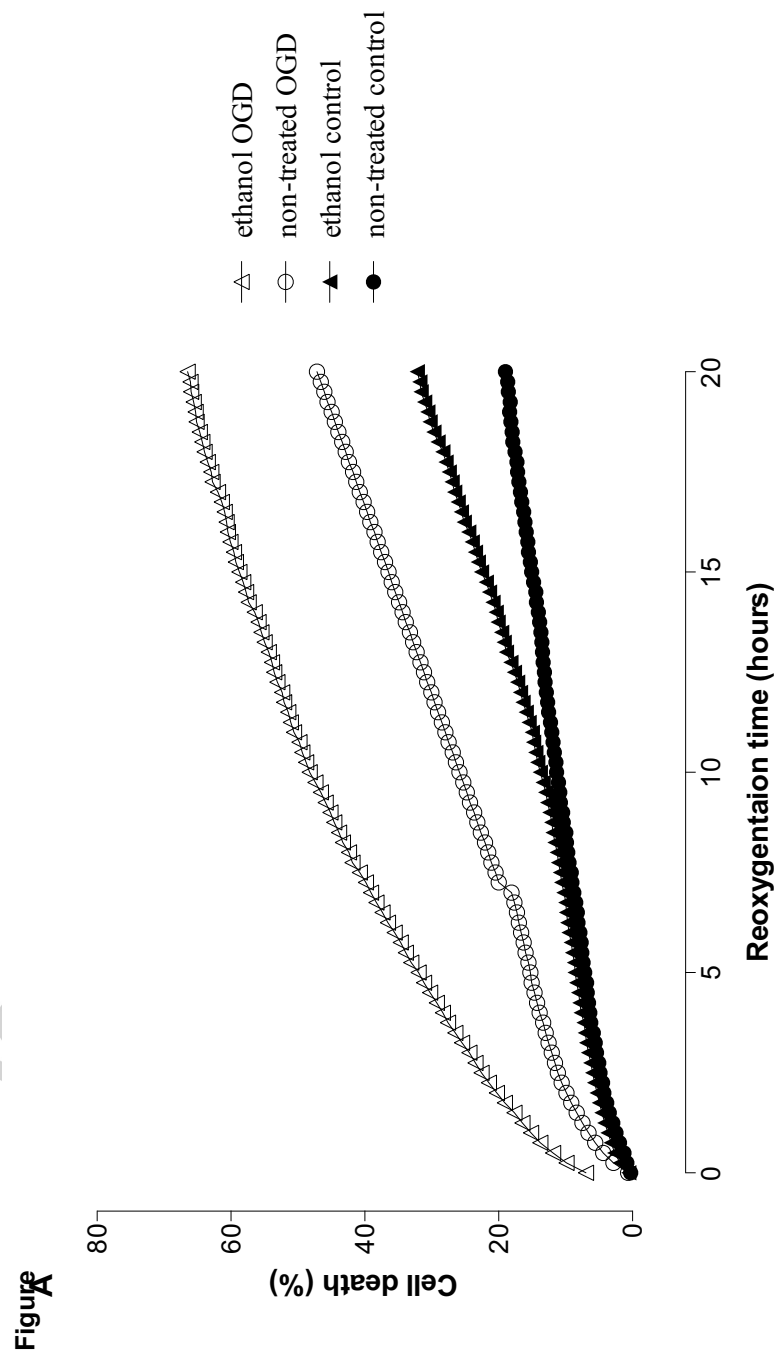
B

non-treated control ethanol control non-treated OGD ethanol OGD









Figure

